



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/720,583
Source: pc/09
Date Processed by STIC: 7/27/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/720,583

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

PCT09

RAW SEQUENCE LISTING

DATE: 07/27/2001

PATENT APPLICATION: US/09/720,583

TIME: 19:46:49

Input Set : A:\Sequence listing US.ST25.txt

Output Set: N:\CRF3\07272001\I720583.raw

3 <110> APPLICANT: DSM N.V.
 4 POUWELS, Pieter
 5 van LUIJK, Nicole
 6 JORE, Johannes
 7 LUITEN, Rudolf
 9 <120> TITLE OF INVENTION: Propionibacterium Vector
 11 <130> FILE REFERENCE: MBHB00-1314
 13 <140> CURRENT APPLICATION NUMBER: US 09/720,583
 C0/c 14 <141> CURRENT FILING DATE: 2001-06-25
 16 <150> PRIOR APPLICATION NUMBER: PCT/EP99/04416
 17 <151> PRIOR FILING DATE: 1999-06-25
 19 <150> PRIOR APPLICATION NUMBER: EP 98305033.7
 20 <151> PRIOR FILING DATE: 1998-06-25
 22 <160> NUMBER OF SEQ ID NOS: 13
 24 <170> SOFTWARE: PatentIn version 3.0

Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES

271 <210> SEQ ID NO: 3
 272 <211> LENGTH: 85
 273 <212> TYPE: PRT
 274 <213> ORGANISM: Propionibacterium freudenreichii LMG16545
 276 <400> SEQUENCE: 3
 277 Met Thr Thr Arg Glu Arg Leu Pro Arg Asn Gly Tyr Ser Ile Ala Ala
 278 1 5 10 15
 280 Ala Ala Lys Lys Leu Gly Val Ser Glu Ser Thr Val Lys Arg Trp Thr
 E--> 281 ~~20~~ 20 25 30
 283 Ser Glu Pro Arg Glu Glu Phe Val Ala Arg Val Ala Ala Arg His Ala
 E--> 284 35 40 45
 286 Arg Ile Arg Glu Leu Arg Ser Glu Gly Gln Ser Met Arg Ala Ile Ala
 E--> 287 50 55 60
 289 Ala Glu Val Gly Val Ser Val Gly Thr Val His Tyr Ala Leu Asn Lys
 E--> 290 65 70 75 80
 291 Asn Arg Thr Asp Ala
 E--> 292 85

*misaligned
 amino acid
 nos. - see item 3
 on Error
 summary
 sheet*

see pgs 2-3 for more errors

720,583. 2

<220>

<221> CDS

<222> (1181)..(1438)

Delete this from sequence 1 - CDS

ends

at 1184

9/720,583 3

<210> 4

<211> 59

<212> DNA

<213> Artificial Sequence

see item 11 on Env Summary Sheet

<400> 4

aattcaagct tgtcgacgtt aacctgcagg catgcggatc cggtagcgat atcagatct 59

FYI
→

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/720,583

DATE: 07/27/2001

TIME: 19:46:50

Input Set : A:\Sequence listing US.ST25.txt

Output Set: N:\CRF3\07272001\I720583.raw

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:125 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 1, CDS
 LOCATION:1181..1438
 L:281 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
 M:332 Repeated in SeqNo=3
 L:299 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:299 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:307 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:307 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:315 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:315 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:323 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:323 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:331 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:331 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:339 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:339 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:349 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:349 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:357 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:357 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:365 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:365 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:373 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:373 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: